

ABSTRACT

The present invention generally relates to a MHC ligand database populated with MHC ligand sequences, motifs, extended motifs, submotifs, ligands unique to infected cells, tumor specific ligands, as well as a collection of current and future developed MHC ligand sequences developed by alternative methods. Other than the ligand sequences developed by alternative methods (which are in many cases non-standardized), the remaining ligand sequences are obtained in a standardized and minimum-variable dependent manner from soluble HLA molecules constructed according to the methodology described herein. The present invention further includes methodologies incorporating linear and predictive algorithm searching and comparison utilities.

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